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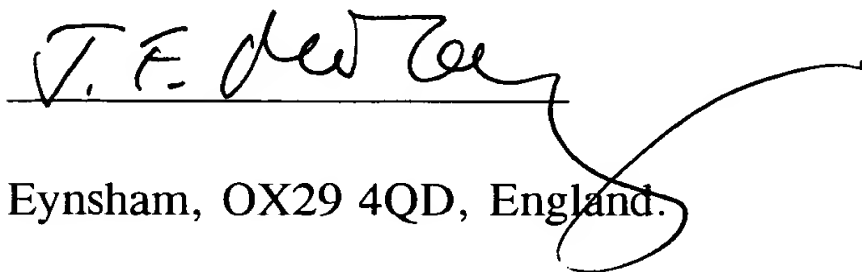
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Signed, this 18th day of September 2004,


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Munich, 21st June 2001
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Faust

New Nucleotide Sequences Coding for the sigD gene

The present invention provides nucleotide sequences of coryneform bacteria coding for the sigD gene and a process for the enzymatic production of amino acids using bacteria
5 in which the sigD gene is enhanced.

Prior Art

L-amino acids are used in human medicine and in the pharmaceutical industry, in the foodstuffs industry and, most especially, in animal nutrition.

10 It is known that amino acids can be produced by fermentation of strains of coryneform bacteria, in particular *Corynebacterium glutamicum*. On account of the great importance of amino acids efforts are constantly being made to improve the production processes. Process
15 improvements may involve fermentation technology measures such as for example stirring and provision of oxygen, or the composition of the nutrient media, such as for example the sugar concentration during the fermentation, or the working-up to the product form by for example ion exchange
20 chromatography or the intrinsic performance properties of the microorganism itself.

In order to improve the performance properties of these microorganisms methods involving mutagenesis, selection and mutant selection are employed. In this way strains are
25 obtained that are resistant to antimetabolites or are auxotrophic for regulatorily important metabolites, and that produce amino acids.

For some years methods of recombinant DNA technology have also been used to improve L-amino acid-producing strains of
30 *corynebacterium*, by amplifying individual amino acid biosynthesis genes and investigating the effect on amino acid production.

Object of the Invention

The inventors have been involved in providing new techniques for the improved enzymatic production of amino acids.

5 Description of the Invention

When L-amino acids or amino acids are mentioned hereinafter, it is understood that this refers to one or more amino acids including their salts, selected from the group L-asparagine, L-threonine, L-serine, L-glutamate,
10 L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine. Lysine is particularly preferred.

The present invention provides an isolated polynucleotide
15 from coryneform bacteria containing a polynucleotide sequence coding for the sigD gene, selected from the group

- a) polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,
- 20 b) polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID No. 2,
- c) polynucleotide that is complementary to the polynucleotides of a) or b), and
- 25 d) polynucleotide containing at least at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),

the polypeptide preferably having the activity of the sigma factor D.

The present invention also provides the aforementioned polynucleotide, which is preferably a replicable DNA containing:

- (i) the nucleotide sequence shown in SEQ ID No. 1, or
- 5 (ii) at least one sequence that corresponds to the sequence (i) within the region of degeneracy of the genetic code, or
- (iii) at least one sequence that hybridises with the sequence that is complementary to the sequence
- 10 (i) or (ii), and optionally
- (iv) functionally neutral sense mutations in (i).

The invention furthermore provides

- a replicable polynucleotide, in particular DNA, containing the nucleotide sequence as shown in SEQ ID No. 1;
- 15 a polynucleotide coding for a polypeptide that contains the amino acid sequence as shown in SEQ ID No. 2;
- a vector containing the polynucleotide according to the invention, in particular a shuttle vector or plasmid vector, and
- 20 coryneform bacteria that contain the vector or in which the sigD gene is enhanced.

- The present invention moreover provides polynucleotides that consist substantially of a polynucleotide sequence that can be obtained by screening by means of hybridisation
- 25 of a corresponding gene library of a coryneform bacterium that contains the complete gene or parts thereof, with a probe that contains the sequence of the polynucleotide of the invention according to SEQ ID No. 1 or a fragment thereof, and isolation of the aforementioned polynucleotide
 - 30 sequence.

Polynucleotides that contain the sequences according to the invention are suitable as hybridisation probes for RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes in their full length that code for the sigma factor D, or to isolate such nucleic acids or polynucleotides or genes that have a high sequence similarity to that of the sigD genes.

Polynucleotides that contain the sequences according to the invention are furthermore suitable as primers with the aid of which, and by employing the polymerase chain reaction (PCR), DNA of genes can be produced that code for the sigma factor D.

Such oligonucleotides serving as probes or primers contain at least 30, preferably at least 20, and most particularly preferably at least 15 successive nucleotides. Also suitable are oligonucleotides with a length of at least 40 or 50 nucleotides.

"Isolated" denotes separated from its natural environment.

"Polynucleotide" refers in general to polyribonucleotides and polydeoxyribonucleotides, which may be unmodified RNA or DNA or modified RNA or DNA.

The polynucleotides according to the invention include a polynucleotide according to SEQ ID No. 1 or a fragment produced therefrom, and also polynucleotides that are at least 70%, preferably at least 80% and particularly preferably at least 90% to 95% identical to the polynucleotide according to SEQ ID No. 1 or a fragment produced therefrom.

The term "polypeptides" is understood to mean peptides or proteins that contain two or more amino acids bound by peptide bonds.

The polypeptides according to the invention include a polypeptide according to SEQ ID No. 2, in particular those with the biological activity of the sigma factor D and also those that are at least 70%, preferably at least 80% and particularly preferably at least 90% to 95% identical to the polypeptide according to SEQ ID No. 2 and that have the aforementioned activity.

The invention furthermore provides a process for the enzymatic production of amino acids selected from the group L-asparagine, L-threonine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine, using coryneform bacteria that in particular already produce amino acids and in which the nucleotide sequences coding for the sigD gene are enhanced, in particular overexpressed.

The term "enhancement" describes in this connection the raising of the intracellular activity of one or more enzymes in a microorganism that are coded by the corresponding DNA, by for example increasing the number of copies of the gene or genes, using a strong promoter, or using a gene that codes for a corresponding enzyme having a high activity, and optionally combining these measures.

The microorganisms that are the subject of the present invention are able to produce L-amino acids from glucose, sucrose, lactose, fructose, maltose, molasses, starch, cellulose or from glycerol and ethanol. The microorganisms may be representatives of coryneform bacteria, in particular of the genus *Corynebacterium*. In the genus *Corynebacterium* there should in particular be mentioned the species *Corynebacterium glutamicum*, which is known to those skilled in the art for its ability to produce L-amino acids.

Suitable strains of the genus *Corynebacterium*, in particular of the species *Corynebacterium glutamicum* (*C. glutamicum*), are in particular the known wild type strains

- 5 *Corynebacterium glutamicum* ATCC13032
- Corynebacterium acetoglutamicum* ATCC15806
- Corynebacterium acetoacidophilum* ATCC13870
- Corynebacterium thermoaminogenes* FERM BP-1539
- Corynebacterium melassecola* ATCC17965
- 10 *Brevibacterium flavum* ATCC14067
- Brevibacterium lactofermentum* ATCC13869 and
- Brevibacterium divaricatum* ATCC14020

and L-amino acid-producing mutants or strains produced therefrom.

- 15 The inventors have successfully isolated from *C. glutamicum* the new sigD gene coding for the enzyme sigma factor D.

In order to isolate the sigD gene or also other genes from *C. glutamicum*, a gene library of this microorganism is first of all incorporated in *Escherichia coli* (*E. coli*).

- 20 The incorporation of gene libraries is described in generally known textbooks and manuals. As examples there may be mentioned the textbook by Winnacker: *Gene and Klone, Eine Einführung in die Gentechnologie* (Verlag Chemie, Weinheim, Germany, 1990) or the manual by Sambrook et al.: *Molecular Cloning, A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1989). A very well-known gene library is
- 25 that of the *E. coli* K-12 strain W3110, which was incorporated by Kohara et al. (*Cell* 50, 495-508 (1987)) into λ vectors. Bathe et al. (*Molecular and General*
- 30 *genetics*, 252:255-265, 1996) describe a gene library of *C. glutamicum* ATCC13032 that has been incorporated by means of the cosmid vector SuperCos I (Wahl et al., 1987, *Proceedings of the National Academy of Sciences USA*,

84:2160-2164) in the *E. coli* K-12 strain NM554 (Raleigh et al., 1988, *Nucleic Acids Research* 16:1563-1575).

Börmann et al. (*Molecular Microbiology* 6(3), 317-326 (1992)) in turn describe a gene library of *C. glutamicum* ATCC13032 using the cosmid pH79 (Hohn and Collins, *Gene* 11, 291-298 (1980)).

In order to produce a gene library of *C. glutamicum* in *E. coli*, there may also be used plasmids such as pBR322 (Bolivar, *Life Sciences*, 25, 807-818 (1979)) or pUC9 (Vieira et al., 1982, *Gene*, 19:259-268). Suitable hosts are in particular those *E. coli* strains that are restriction-defective and recombinant-defective. An example of such is the strain DH5 α mcr, which has been described by Grant et al. (*Proceedings of the National Academy of Sciences USA*, 87 (1990) 4645-4649). The long DNA fragments cloned with the aid of cosmids can in turn then be subcloned into common vectors suitable for the sequencing and subsequently sequenced, as is described for example by Sanger et al. (*Proceedings of the National Academy of Sciences of the United States of America*, 74:5463-5467, 1977).

The DNA sequences obtained can then be investigated using known algorithms or sequence analysis programs, such as for example that of Staden (*Nucleic Acids Research* 14, 217-232(1986)), that of Marck (*Nucleic Acids Research* 16, 1829-1836 (1988)) or the GCG program of Butler (*Methods of Biochemical Analysis* 39, 74-97 (1998)).

The new DNA sequence of *C. glutamicum* coding for the sigD gene was obtained in this way, and as SEQ ID No. 1 is part of the present invention. The amino acid sequence of the corresponding protein was also derived from the existing DNA sequence using the aforescribed methods. The resultant amino acid sequence of the sigD gene product is shown in SEQ ID No. 2.

Coding DNA sequences that result from SEQ ID No. 1 due to the degeneracy of the genetic code are likewise covered by the present invention. Similarly, DNA sequences that hybridise with SEQ ID No. 1 or parts of SEQ ID No. 1 are also part of the invention. In the specialist field conservative amino acid replacements, such as for example the replacement of glycine by alanine or of aspartic acid by glutamic acid, in proteins are furthermore known as sense mutations that do not lead to any basic change in the activity of the protein, i.e. are functionally neutral. It is furthermore known that changes at the N-end and/or C-end of a protein do not significantly impair their function or indeed may even stabilise their function. The person skilled in the art can find relevant information on this in, *inter alia*, Ben-Bassat et al. (Journal of Bacteriology 169:751-757 (1987)), in O'Regan et al. (Gene 77:237-251 (1989)), in Sahin-Toth et al. (Protein Sciences 3:240-247 (1994)), in Hochuli et al. (Bio/Technology 6:1321-1325 (1988)) and in known textbooks and manuals on genetics and molecular biology. Amino acid sequences that are obtained in a corresponding manner from SEQ ID No. 2 are likewise covered by the invention.

In the same way, DNA sequences that hybridise with SEQ ID No. 1 or parts of SEQ ID No. 1 are also covered by the invention. Finally, DNA sequences that are produced by the polymerase chain reaction (PCR) using primers resulting from SEQ ID No. 1, are also part of the invention. Such oligonucleotides typically have a length of at least 15 nucleotides.

The person skilled in the art can find information on the identification of DNA sequences by means of hybridisation in, *inter alia*, the manual "The DIG System User's Guide for Filter Hybridization" published by Boehringer Mannheim GmbH (Mannheim, Germany, 1993) and in Liebl et al. (International Journal of Systematic Bacteriology (1991))

41: 255-260). The hybridisation takes place under strict conditions, in other words only hybrids are formed in which the probe and target sequence, i.e. the polynucleotides treated with the probe, are at least 70% identical. It is known that the strictness of the hybridisation conditions including the washing step is influenced or determined by varying the buffer composition, temperature and the salt concentration. The hybridisation reaction is preferably carried out under conditions that are relatively less strict compared to the wash steps (Hybaid Hybridisation Guide, Hybaid Limited, Teddington, UK, 1996).

For the hybridisation reaction there may for example be used a 5x SSC buffer at a temperature of ca. 50 - 68°C. In this connection probes can also hybridise with polynucleotides that are less than 70% identical to the probe sequence. Such hybrids are less stable and are removed by washing under stringent conditions. This may be achieved for example by reducing the salt concentration to 2x SSC and then if necessary to 0.5x SSC (The DIG System User's Guide for Filter Hybridisation, Boehringer Mannheim, Mannheim, Germany, 1995), a temperature of ca. 50 - 68°C being established. It is also possible to reduce the salt concentration down to 0.1x SSC. By stepwise raising of the hybridisation temperature in steps of ca. 1 - 2°C from 50 to 68°C, polynucleotide fragments can be isolated that are for example at least 70% or at least 80% or even at least 90% to 95% identical to the sequence of the probe that is used. Further details relating to hybridisation may be obtained in the form of so-called kits available on the market (e.g. DIG Easy Hyb from Roche Diagnostics GmbH, Mannheim, Germany, Catalog No. 1603558).

The person skilled in the art can find details on the amplification of DNA sequences by means of the polymerase chain reaction (PCR) in, *inter alia*, the manual by Gait: Oligonucleotides Synthesis: A Practical Approach (IRL

Press, Oxford, UK, 1984) and in Newton and Graham: PCR (Spektrum Akademischer Verlag, Heidelberg, Germany, 1994).

In the course of work carried out in connection with the present invention it was established that coryneform
5 bacteria after overexpression of the sigD gene produce amino acids in an improved manner.

In order to achieve an overexpression the number of copies of the corresponding genes can be increased, or alternatively the promoter and regulation region or the
10 ribosome binding site located upstream of the structure gene can be mutated. Expression cassettes that are incorporated upstream of the structure gene act in the same way. By means of inducible promoters it is in addition possible to increase the expression in the course of the
15 enzymatic amino acid production. The expression is similarly improved by measures aimed at prolonging the lifetime of the m-RNA. Furthermore, the enzyme activity is also enhanced by preventing the degradation of the enzyme protein. The genes or gene constructs may either be
20 present in plasmids having different numbers of copies, or may be integrated and amplified in the chromosome. Alternatively, an overexpression of the relevant genes may furthermore be achieved by altering the composition of the media and the culture conditions.

25 The person skilled in the art can find details on the above in, *inter alia*, Martin et al. (Bio/Technology 5, 137-146 (1987)), in Guerrero et al. (Gene 138, 35-41 (1994)), Tsuchiya and Morinaga (Bio/Technology 6, 428-430 (1988)), in Eikmanns et al. (Gene 102, 93-98 (1991)), in European
30 Patent Specification 0 472 869, in US Patent 4,601,893, in Schwarzer and Pühler (Bio/Technology 9, 84-87 (1991)), in Reinscheid et al. (Applied and Environmental Microbiology 60, 126-132 (1994)), in LaBarre et al. (Journal of Bacteriology 175, 1001-1007 (1993)), in Patent Application
35 WO 96/15246, in Malumbres et al. (Gene 134, 15 - 24

(1993)), in Japanese laid open Specification JP-A-10-229891, in Jensen and Hammer (Biotechnology and Bioengineering 58, 191-195 (1998)), in Makrides (Microbiological Reviews 60:512-538 (1996)) and in known
5 textbooks on genetics and molecular biology.

For the enhancement the sigD gene according to the invention was overexpressed for example by means of episomal plasmids. Suitable plasmids are those that are replicated in coryneform bacteria. Numerous known plasmid
10 vectors, such as for example pZ1 (Menkel et al., Applied and Environmental Microbiology (1989) 64: 549-554), pEKEx1 (Eikmanns et al., Gene 102:93-98 (1991)) or pHS2-1 (Sonnen et al., Gene 107:69-74 (1991)) are based on the cryptic plasmids pHM1519, pBL1 or pGA1. Other plasmid vectors,
15 such as for example those based on pCG4 (US-A 4,489,160), or pNG2 (Serwold-Davis et al., FEMS Microbiology Letters 66, 119-124 (1990)), or pAG1 (US-A 5,158,891) may be used in a similar way.

Furthermore, also suitable are those plasmid vectors with
20 the aid of which the process of gene amplification by integration in the chromosome can be employed, such as has been described for example by Reinscheid et al. (Applied and Environmental Microbiology 60, 126-132 (1994)) for the duplication and amplification of the hom-thrB operon. In
25 this method the complete gene is cloned into a plasmid vector that can replicate in a host (typically E. coli) but not in C. glutamicum. Suitable vectors are for example pSUP301 (Simon et al., Bio/Technology 1, 784-791 (1983)), pK18mob or pK19mob (Schäfer et al., Gene 145, 69-73
30 (1994)), pGEM-T (Promega Corporation, Madison, WI, USA), pCR2.1-TOPO (Shuman (1994). Journal of Biological Chemistry 269:32678-84; US-A 5,487,993), pCR®Blunt (Invitrogen, Groningen, Netherlands; Bernard et al., Journal of Molecular Biology, 234: 534-541 (1993)), pEM1 (Schrumpf et
35 al., 1991, Journal of Bacteriology 173:4510-4516) or pBGS8

(Spratt et al., 1986, Gene 41: 337-342). The plasmid vector that contains the gene to be amplified is then transferred by conjugation or transformation into the desired strain of *C. glutamicum*. The method of conjugation
5 is described for example in Schäfer et al. (Applied and Environmental Microbiology 60, 756-759 (1994)). Transformation methods are described for example in Thierbach et al. (Applied Microbiology and Biotechnology 29, 356-362 (1988)), Dunican and Shivnan (Bio/Technology 7,
10 1067-1070 (1989)) and Tauch et al. (FEMS Microbiological Letters 123, 343-347 (1994)). After homologous recombination by means of a crossover event, the resulting strain contains at least two copies of the relevant gene.

In addition it may be advantageous for the production of L-
15 amino acids to enhance, in particular to overexpress, in addition to the *sigD* gene also one or more enzymes of the respective biosynthesis pathway, glycolysis, anaplerosis, citric acid cycle, pentose phosphate cycle, amino acid export and optionally regulatory proteins.

20 Thus for example, for the production of L-amino acids, in addition to the enhancement of the *sigD* gene one or more genes selected from the following group may be enhanced, in particular overexpressed:

- the gene *dapA* coding for dihydrodipicolinate synthase
25 (EP-B 0 197 335),
- the gene *gap* coding for glyceraldehyde-3-phosphate dehydrogenase (Eikmanns (1992), Journal of Bacteriology 174:6076-6086),
- the gene *tpi* coding for triosephosphate isomerase
30 (Eikmanns (1992), Journal of Bacteriology 174:6076-6086),
- the gene *pgk* coding for 3-phosphoglycerate kinase (Eikmanns (1992), Journal of Bacteriology 174:6076-6086),

- the gene zwf coding for glucose-6-phosphate dehydrogenase (JP-A-09224661),
- the gene pyc coding for pyruvate carboxylase (DE-A-198 31 609),
- 5 • the gene mgo coding for malate-quinone-oxidoreductase (Molenaar et al., European Journal of Biochemistry 254, 395-403 (1998)),
- the gene lysC coding for a feedback-resistant aspartate kinase (Accession No.P26512),
- 10 • the gene lysE coding for lysine export (DE-A-195 48 222),
- the gene hom coding for homoserine dehydrogenase (EP-A 0131171),
- the gene ilvA coding for threonine dehydratase (Möckel et al., Journal of Bacteriology (1992) 8065-8072)) or the
- 15 allele ilvA(Fbr) coding for a feedback-resistant threonine dehydratase (Möckel et al., (1994) Molecular Microbiology 13: 833-842),
- the gene ilvBN coding for acetohydroxy acid synthase (EP-B 0356739),
- 20 • the gene ilvD coding for dihydroxy acid dehydratase (Sahm and Eggeling (1999) Applied and Environmental Microbiology 65: 1973-1979),
- the gene zwal coding for the Zwal protein (DE: 19959328.0, DSM 13115).
- 25 Furthermore, it may be advantageous for the production of L-amino acids, in addition to the enhancement of the sigD genes also to attenuate, in particular to reduce, the expression of one or more genes selected from the group

- the gene pck coding for phosphoenol pyruvate carboxykinase (DE 199 50 409.1; DSM 13047),
- the gene pgi coding for glucose-6-phosphate isomerase (US 09/396,478; DSM 12969),
- 5 • the gene poxB coding for pyruvate oxidase (DE: 1995 1975.7; DSM 13114),
- the gene zwa2 coding for the Zwa2 protein (DE: 19959327.2, DSM 13113).

In addition it may be advantageous for the production of
10 amino acids, in addition to the overexpression of the sigD
gene also to switch off undesirable secondary reactions
(Nakayama: "Breeding of Amino Acid Producing Micro-
organisms", in: Overproduction of Microbial Products,
Krumphanzl, Sikyta, Vanek (eds.), Academic Press, London,
15 UK, 1982).

The microorganisms produced according to the invention are
likewise the subject of the invention and may be cultivated
continuously or batchwise in a batch process (batch
cultivation) or in a fed batch process (feed process) or
20 repeated fed batch process (repetitive feed process) for
the purposes of production of amino acids. A summary of
known cultivation methods is given in the textbook by Chmiel
(Bioprozeßtechnik 1. Einführung in die Bioverfahrenstechnik
(Gustav Fischer Verlag, Stuttgart, 1991)) or in the
25 textbook by Storhas (Bioreaktoren und periphere
Einrichtungen (Vieweg Verlag, Brunswick/Wiesbaden, 1994)).

The culture medium to be used must suitably satisfy the
requirements of the relevant strains. Descriptions of
culture media for various microorganisms are given in the
30 manual "Manual of Methods for General Bacteriology" of the
American Society for Bacteriology (Washington D.C., USA,
1981).

Carbon sources that may be used include sugars and carbohydrates such as for example glucose, sucrose, lactose, fructose, maltose, molasses, starch and cellulose, oils and fats such as for example soya bean oil, sunflower oil, peanut oil and coconut oil, fatty acids such as for example palmitic acid, stearic acid and linoleic acid, alcohols such as for example glycerol and ethanol, and organic acids such as for example acetic acid. These substances may be used individually or as a mixture.

10 Nitrogen sources that may be used include organic nitrogen-containing compounds such as peptones, yeast extract, meat extract, malt extract, corn steep liquor, soya bean flour and urea, or inorganic compounds such as ammonium sulfate, ammonium chloride, ammonium phosphate, ammonium carbonate
15 and ammonium nitrate. The nitrogen sources may be used individually or as a mixture.

Phosphorus sources that may be used include phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium salts. The culture medium must furthermore contain salts of metals, such as for example magnesium sulfate or iron sulfate, that are necessary for growth. Finally, essential growth promoters such as amino acids and vitamins may be used in addition to the aforementioned substances. Suitable
20 precursors may furthermore be added to the culture medium. The aforementioned starting substances may be added to the culture in the form of a single one-off batch, or may be suitably metered in during the culture process.

Basic compounds such as sodium hydroxide, potassium hydroxide, ammonia or ammonia water, or acidic compounds such as phosphoric acid or sulfuric acid, are used in a suitable manner in order to control the pH of the culture. Anti-foaming agents such as for example fatty acid polyglycol esters may be used to control foam formation.
30 In order to maintain the stability of plasmids suitable

selectively acting substances such as for example antibiotics may be added to the medium. In order to maintain aerobic conditions, oxygen or oxygen-containing gas mixtures such as for example air are introduced into the culture. The temperature of the culture is normally 20°C to 45°C and preferably 25°C to 40°C. The culture is continued until a maximum of the desired product has been formed. This objective is normally achieved within 10 hours to 160 hours.

- 10 Methods for the determination of L-amino acids are known to the person skilled in the art. The analysis may be carried out for example as described by Spackman et al. (Analytical Chemistry, 30, (1958), 1190) by ion exchange chromatography followed by ninhydrin derivatisation, or can be carried out
15 by reversed phase HPLC, as described by Lindroth et al. (Analytical Chemistry (1979) 51: 1167-1174).

The process according to the invention serves for the enzymatic production of amino acids.

- The present invention is described in more detail
20 hereinafter with the aid of examples of implementation.

- The isolation of plasmid DNA from Escherichia coli as well as all techniques involved in restriction, Klenow treatment and alkaline phosphatase treatment have been carried out by Sambrook et al. (Molecular Cloning. A Laboratory Manual
25 (1989) Cold Spring Harbour Laboratory Press, Cold Spring Harbor, NY, USA). Methods for the transformation of Escherichia coli are also described in this manual.

- The composition of readily available nutrient media such as LB or TY media are also given in the manual by Sambrook et
30 al.

Example 1

Production of a genomic cosmid gene library from
Corynebacterium glutamicum ATCC 13032

Chromosomal DNA from *Corynebacterium glutamicum* ATCC 13032
5 was isolated as described by Tauch et al. (1995, Plasmid
33:168-179) and partially cleaved with the restriction
enzyme Sau3AI (Amersham Pharmacia, Freiburg, Germany,
product description Sau3AI, Code no. 27-0913-02). The DNA
fragments were desphosphorylated with shrimp alkaline
10 phosphatase (Roche Diagnostics GmbH, Mannheim, Germany,
product description SAP, Code no. 1758250). The DNA of the
cosmid vector SuperCos1 (Wahl et al. (1987) Proceedings of
the National Academy of Sciences USA 84:2160-2164),
obtained from Stratagene (La Jolla, USA, product
15 description SuperCos1 Cosmid Vector Kit, Code no. 251301)
was cleaved with the restriction enzyme XbaI (Amersham
Pharmacia, Freiburg, Germany, product description XbaI,
Code no. 27-0948-02) and likewise dephosphorylated with
shrimp alkaline phosphatase.

20 The cosmid DNA was then cleaved with the restriction enzyme
BamHI (Amersham Pharmacia, Freiburg, Germany, product
description BamHI, Code no. 27-0868-04). The cosmid DNA
treated in this way was mixed with the treated ATCC13032-
DNA and the batch was treated with T4-DNA ligase (Amersham
25 Pharmacia, Freiburg, Germany, product description T4-DN
ligase, Code no. 27-0870-04). The ligation mixture was
then packed into phages using the Gigapack II XL Packing
Extracts (Stratagene, La Jolla, USA, product description
Gigapack II XL Packing Extract, Code no. 200217).

30 For the infection of the *E. coli* strain NM554 (Raleigh et
al. 1988, Nucleic Acid Research 16:1563-1575) the cells
were taken up in 10 mM MgSO₄ and mixed with an aliquot of
the phage suspension. Infection and titration of the
cosmid library were carried out as described by Sambrook et

al. (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor), the cells having been plated out on LB agar (Lennox, 1955, Virology, 1:190) with 100 mg/l ampicillin. Recombinant individual clones were selected after
5 incubation overnight at 37°C.

Example 2

Isolation and sequencing of the sigD gene

The cosmid DNA of an individual colony was isolated using the Qiaprep Spin Miniprep Kit (Product No. 27106, Qiagen, Hilden, Germany) according to the manufacturer's
10 instructions and partially cleaved with the restriction enzyme Sau3AI (Amersham Pharmacia, Freiburg, Germany, product description Sau3AI, Product No. 27-0913-02). The DNA fragments were dephosphorylated with shrimp alkaline
15 phosphatase (Roche Diagnostics GmbH, Mannheim, Germany, product description SAP, Product No. 1758250). After gel electrophoresis separation, the cosmid fragments were isolated in an order of magnitude of 1500 to 2000 bp using the QiaExII Gel Extraction Kit (Product No. 20021, Qiagen,
20 Hilden, Germany).

The DNA of the sequencing vector pZero-1, obtained from Invitrogen (Groningen, Netherlands, product description Zero Background Cloning Kit, Product No. K2500-01), was cleaved with the restriction enzyme BamHI (Amersham
25 Pharmacia, Freiburg, Germany, product description BamHI, Product No. 27-0868-04). The ligation of the cosmid fragments in the sequencing vector pZero-1 was carried out as described by Sambrook et al. (1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor), the DNA mixture
30 having been incubated overnight with T4 ligase (Pharmacia Biotech, Freiburg, Germany). This ligation mixture was then electroporated (Tauch et al. 1994, FEMS Microbiol Letters, 123:343-7) into the E. coli strain DH5 α MCR (Grant, 1990, Proceedings of the National Academy of Sciences

U.S.A., 87:4645-4649) and plated out onto LB agar (Lennox, 1955, Virology, 1:190) with 50 mg/l zeocin.

The plasmid preparation of the recombinant clone was performed with the Biorobot 9600 (Product No. 900200, 5 Qiagen, Hilden, Germany). The sequencing was carried out according to the dideoxy chain termination method of Sanger et al. (1977, Proceedings of the National Academy of Sciences U.S.A., 74:5463-5467) as modified by Zimmermann et al. (1990, Nucleic Acids Research, 18:1067). The "RR 10 dRhodamin Terminator Cycle Sequencing Kit" of PE Applied Biosystems (Product No. 403044, Weiterstadt, Germany) was used. The gel electrophoresis separation and analysis of the sequencing reaction was carried out in a "rotiphoresis NF acrylamide/bisacrylamide" gel (29:1) (Product No. 15 A124.1, Roth, Karlsruhe, Germany) using the "ABI Prism 377" sequencing apparatus from PE Applied Biosystems (Weiterstadt, Germany).

The raw sequencing data obtained were then processed using the Staden program package (1986, Nucleic Acids Research, 20 14:217-231) Version 97-0. The individual sequences of the pZerol derivatives were assembled into a coherent contig. The computer-assisted coding region analysis was prepared using the XNIP program (Staden, 1986, Nucleic Acids Research, 14:217-231).

25 The nucleotide sequence obtained is shown in SEQ ID No. 1. The analysis of the nucleotide sequence revealed an open reading frame of 567 base pairs, which was termed the sigD gene. The sigD gene codes for a protein of 188 amino acids.

SEQUENCING PROTOCOL

<110> Degussa-Hüls AG

5 <120> New nucleotide sequences coding for the sigD gene

<130> bbbbbb BT

<140>

10 <141>

<160> 2

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 1129

<212> DNA

<213> Corynebacterium glutamicum

20

<220>

<221> CDS

<222> (301)..(864)

<223> sigD-Gen

25

<400> 1

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aatctccggt gaattcttat agataacttg tttttgcagg tcaggacggg gttaagggga 120

30

tgggtgttat ctgtcagtat gtgaggagat caaggtgttg ggggttctag ttgctaagat 180

ggtgaaaacc cgtgaggcca aaatccaact ggggtgaatta cccctgcata aatgcatgag 240

35

ggctttatac ttgtcttatt attaaacttt taggggttttg atgcaggaag gtgcgagaac 300

ttg gct gat act gag cgc gag ctg gct gac ctg gta ccg cag gca acg 348

Met Ala Asp Thr Glu Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr

1 5 10 15

40

gcg ggc gat cgt cgg gca ttg caa aga ata atg gag att att cac ccc 396

Ala Gly Asp Arg Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro

20 25 30

45

att gtt ttg cgt tat gct cgc gct cgt att gga ggt gga cgc cag cca 444

Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro

35 40 45

50

acg gca gaa gac gtt gct caa gaa atc tgc ctg gcg gta gcc acc tcc 492

Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser

50 55 60

55

att agg aac ttt gtc gac cag ggt agg ccg ttc atg gcg ttt gtc tac 540

Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr

65 70 75 80

ggc att gca tct aac aag gtc gca gat gct cac agg gcg atg tcg agg 588

Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg

85 90 95

gat aaa tcg act cct att gag gaa gtc cca gaa act tca cca gat act 636
 Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr
 100 105 110

5

ttt acc ccc gaa gac ttt gcg ctg gtc agc gat gga agt aac aga gtt 684
 Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val
 115 120 125

10

agg gaa ctt ctc gat cta ctg agt gaa aag gca cgc gac att ctt atc 732
 Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile
 130 135 140

15

ttg aga gtt atc gtt ggt ctt tcc gca gaa gaa act gca gag atg gtg 780
 Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val
 145 150 155 160

20

ggc agc acc cca ggt gct gta cga gtt gcc caa cac agg gca ctc acg 828
 Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr
 165 170 175

25

aca ctt cga agc aca ctt gag cag cag gag aac aag taatgactcg 874
 Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys
 180 185

30

acgtctacat ggtggtgagc aggatggcca ggaacacggt aaaggacagc taaagcagct 934
 gttcgacgac gacgcgttct tgactgacct gtcccgcggc gttgatccct cagagggcga 994
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35

<210> 2
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 <212> PRT
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40

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 1 5 10 15

45

Ala Gly Asp Arg Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro
 20 25 30

50

Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro
 35 40 45

Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser
 50 55 60

55

Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr
 65 70 75 80

Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg
 85 90 95

20

Patent Claims

1. Isolated polynucleotide from coryneform bacteria containing a polynucleotide sequence coding for the sigD gene, selected from the group
- 5
- a) polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,
- b) polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to the amino acid sequence of SEQ ID No. 2,
- 10
- c) polynucleotide that is complementary to the polynucleotides of a) or b), and
- d) polynucleotide containing at least at least 15 successive nucleotides of the polynucleotide sequence of a), b) or c),
- 15
- the polypeptide preferably having the activity of the sigma factor D.
- 20 2. Polynucleotide as claimed in claim 1, wherein the polynucleotide is a preferably recombinant DNA replicable in coryneform bacteria.
3. Polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.
- 25 4. Polynucleotide as claimed in claim 2, containing the nucleic acid sequence as shown in SEQ ID No. 1.
5. Replicable DNA as claimed in claim 2, containing
- (i) the nucleotide sequence shown in SEQ ID No. 1, or

- (ii) at least one sequence that corresponds to the sequence (i) within the region of degeneracy of the genetic code, or
 - (iii) at least one sequence that hybridises with the sequence that is complementary to the sequence (i) or (ii), and optionally
 - (iv) functionally neutral sense mutations in (i).
6. Replicable DNA as claimed in claim 5, wherein the hybridisation of sequence (iii) is carried out under conditions of stringency corresponding at most to 2x SSC.
7. Polynucleotide sequence as claimed in claim 2, that codes for a polypeptide that contains the amino acid sequence shown in SEQ ID No. 2.
8. Coryneform bacteria, in which the sigD gene is enhanced, in particular is overexpressed.
9. Process for the enzymatic production of L-amino acids, in particular lysine, wherein the following steps are carried out:
- a) fermentation of the coryneform bacteria producing the desired L-amino acid, in which at least the sigD gene or nucleotide sequences coding for the latter are enhanced, in particular are overexpressed;
 - b) enrichment of the L-amino acid in the medium or in the cells of the bacteria, and
 - c) isolation of the L-amino acid.
10. Process as claimed in claim 9, wherein bacteria are used in which in addition further genes of the

biosynthesis pathway of the desired L-amino acid are enhanced.

11. Process as claimed in claim 9, wherein bacteria are used in which the metabolic pathways that reduce the formation of the desired L-amino acid are at least partially switched off.
12. Process as claimed in claim 9, wherein a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigD gene.
13. Process as claimed in claim 9, wherein the expression of the polynucleotide(s) that codes for the sigD gene is enhanced, in particular is overexpressed.
14. Process as claimed in claim 8, wherein the regulatory properties of the polypeptide (enzyme protein) for which the polynucleotide sigD codes are raised.
15. Process as claimed in claim 9, wherein for the production of L-amino acids coryneform microorganisms are fermented, in which at the same time one or more of the genes selected from the following group is enhanced or overexpressed:
 - 15.1 the gene dapA coding for dihydrodipicolinate synthase,
 - 15.2 the gene gap coding for glyceraldehyde-3-phosphate dehydrogenase,
 - 15.3 the gene tpi coding for triosephosphate isomerase,
 - 15.4 the gene pgk coding for 3-phosphoglycerate kinase,

- 15.5 the gene zwf coding for glucose-6-phosphate dehydrogenase,
- 15.6 the gene pyc coding for pyruvate carboxylase,
- 5 15.7 the gene mqo coding for malate-quinone-oxidoreductase,
- 15.8 the gene lysC coding for a feedback-resistant aspartate kinase,
- 15.9 the gene lysE coding for lysine export,
- 10 15.10 the gene hom coding for homoserine dehydrogenase,
- 15.11 the gene ilvA coding for threonine dehydratase or the allele ilvA(Fbr) coding for a feedback-resistant threonine dehydratase,
- 15 15.12 the gene ilvBN coding for acetohydroxy acid synthase,
- 15.13 the gene ilvD coding for dihydroxy acid dehydratase,
- 15.14 the gene zwal coding for the Zwal protein.
- 20 16. Process as claimed in claim 9, wherein for the production of L-amino acids coryneform microorganisms are fermented in which at the same time one or more of the genes selected from the following group is/are attenuated:
- 25 16.1 the gene pck coding for phosphoenol pyruvate carboxykinase,
- 16.2 the gene pgi coding for glucose-6-phosphate isomerase,

16.3 the gene *poxB* coding for pyruvate oxidase,

16.4 the gene *zwa2* coding for the Zwa2 protein.

17. Coryneform bacteria containing a vector that carries a polynucleotide as claimed in claim 1.

5 18. Process as claimed in one or more of the preceding claims, wherein microorganisms of the genus *Corynebacterium* are used.

10 19. Process for discovering RNA, cDNA and DNA in order to isolate nucleic acids or polynucleotides or genes that code for the sigma factor D or that have a high degree of similarity to the sequence of the *sigD* gene, wherein the polynucleotide containing the polynucleotide sequences as claimed in claims 1, 2, 3 or 4 is used as hybridisation probes.

15

Abstract

The invention relates to an isolated polynucleotide containing a polynucleotide sequence selected from the group

- 5 a) polynucleotide that is at least 70% identical to a polynucleotide coding for a polypeptide that contains the amino acid sequence of SEQ ID No. 2,
- b) polynucleotide coding for a polypeptide that contains an amino acid sequence that is at least 70% identical to
10 the amino acid sequence of SEQ ID No. 2,
- c) polynucleotide that is complementary to the polynucleotides of a) or b), and
- d) polynucleotide containing at least at least 15
15 successive nucleotides of the polynucleotide sequence of a), b) or c),

and a process for the enzymatic production of L-amino acids using coryneform bacteria in which at least the sigD gene is present in enhanced form, and the use of polynucleotides that contain the sequences according to the invention as
20 hybridisation probes.